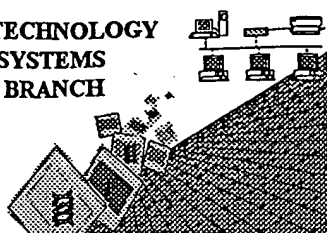# RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/806,368 β_

Source: _PG/09_

Date Processed by STIC: _5/14/2002_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.1 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
                Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 09/806,368B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1_____ Wrapped Nucleics
Wrapped Aminos

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2_____ Invalid Line Length

The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ✓ Misaligned Amino
Numbering

The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4_____ Non-ASCII

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5_____ Variable Length

Sequence(s)_____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6_____ PatentIn 2.0
"bug"

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7_____ Skipped Sequences
(OLD RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8_____ Skipped Sequences
(NEW RULES)

Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9_____ Use of n's or Xaa's
(NEW RULES)

Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10_____ Invalid <213>
Response

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial-Sequence

11_____ Use of <220>

Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

12_____ PatentIn 2.0
"bug"

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13_____ Misuse of n

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

PCT09

pp 1-6
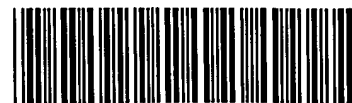
RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/806,368B

DATE: 05/14/2002
TIME: 16:26:47

Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

Does Not Comply
delete - do not insert **Corrected Diskette Needed**
Page numbers in the computer readable form

```
W--> 6  WO 00/21998 PCT/IB99/01621        delete
W--> 8  1
     13 <110> APPLICANT: Hoechst Marion Roussel
     15 <120> TITLE OF INVENTION: MATURE PROTEIN HAVING ANTAGONIST ACTIVITY AGAINST BONE
     16       MORPHOGENETIC PROTEIN.
     18 <130> FILE REFERENCE: JH98KO11 PCT SEQUENCES IN ENGLISH
     20 <140> CURRENT APPLICATION NUMBER: US/09/806,368B
     21 <141> CURRENT FILING DATE: 2001-03-28
     23 <150> PRIOR APPLICATION NUMBER: 10-288103
     24 <151> PRIOR FILING DATE: 1998-10-09
     26 <160> NUMBER OF SEQ ID NOS: 7
     28 <170> SOFTWARE: PatentIn Ver. 2.1
```

(Per Sequence Rules)

ERRORED SEQUENCES

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     30 <210> SEQ ID NO: 1
     31 <211> LENGTH: 119
     32 <212> TYPE: PRT
     33 <213> ORGANISM: Human
     35 <220> FEATURE:
     36 <221> NAME/KEY: CHAIN
     37 <222> LOCATION: (1)..(119)
     38 <223> OTHER INFORMATION: Mature MP52
     40 <300> PUBLICATION INFORMATION:
     41 <301> AUTHORs: MAKISHIMA, Fusoa
     42       TAKAMATSU, Hiroyuki
     43       MIKI, Hideo
     44       KAWAI, Shinji
     45       KIMURA, Michio
     46       MATSUMOTO, Tomoaki
     47       KATSUURA, Mieko
     48       ENOMOTO, Koichi
     65       O 00/21998 PCT/IB99/01621        delete
     67       2
     69       SATOH, Yusuke
     70 <302> TITLE: Novel protein and process for producing the same.
     71 <310> PATENT DOC NO: WO 96/33215
W--> 72 <312> PUBLICATION DATE: (1996-1-0-24)  1996-10-24
     73 <313> RELEVANT RESIDUES: 1 TO 119
     75 <400> SEQUENCE: 1
     77       Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
E--> 78       1              5              10  /10                 15
```

misaligned amino acid number - see item 3 on Error Summary Sheet

5/14/02

RAW SEQUENCE LISTING   DATE: 05/14/2002
PATENT APPLICATION: US/09/806,368B   TIME: 16:26:47

Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

```
 80      Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
 81              20                      25                  30
 83      Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
 84              35                      40                  45
 86      Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
 87          50                      55                  60
 89      Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
 90       65                  70                  75                  80
 92      Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
 93                      85                  90                  95
 95      Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
 96                  100                     105                 110
 98      Val Glu Ser Cys Gly Cys Arg
 99              115
101 <210> SEQ ID NO: 2
102 <211> LENGTH: 114
103 <212> TYPE: PRT
104 <213> ORGANISM: Human
```

W--> 123 WO 00/21998 PCT/IB99/01621   *delete*
W--> 125 3

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128 <220> FEATURE:
129 <221> NAME/KEY: CHAIN
130 <222> LOCATION: (1)..(114)
131 <223> OTHER INFORMATION: Mature BMP-2
133 <300> PUBLICATION INFORMATION:
134 <301> AUTHORs: WANG, Elizabeth A.
135         WOZNEY, John M.
136         ROSEN, Vicki A.
137 <302> TITLE: Novel osteoinductive compositions.
138 <310> PATENT DOC NO: WO 88/00205
139 <312> PUBLICATION DATE: 1988-01-14
140 <313> RELEVANT RESIDUES: 1 TO 114
142 <400> SEQUENCE: 2
144     Gln Ala Lys His Lys Gln Arg Lys Arg Leu Lys Ser Ser Cys Lys Arg
145          1               5                   10                  15
147     His Pro Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp Trp Ile
148              20                      25                  30
150     Val Ala Pro Pro Gly Tyr His Ala Phe Tyr Cys His Gly Glu Cys Pro
151              35                      40                  45
153     Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile Val Gln
```
E--> 154   ~~50~~ 50   ~~55~~ 55   60   *← misaligned amino acid nos.*
```
156     Thr Leu Val Asn Ser Val Asn Ser Lys Ile Pro Lys Ala Cys Cys Val
```
E--> 157   65   70   75   80
```
159     Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu Asn Glu
```
E--> 160   85   90   95
```
162     Lys Val Val Leu Lys Asn Tyr Gln Asp Met Val Val Glu Gly Cys Gly
```
163   ~~100~~ 100   ~~105~~ 105   ~~110~~ 110   *← same error*
E--> 164   Cys Arg
181 WO 00/21998   PCT/IB99/01621   *delete*

(4) delete

```
E--> 184
     187 <210> SEQ ID NO: 3
     188 <211> LENGTH: 116
     189 <212> TYPE: PRT
     190 <213> ORGANISM: Human
     192 <220> FEATURE:
     193 <221> NAME/KEY: CHAIN
     194 <222> LOCATION: (1)..(116)
     195 <223> OTHER INFORMATION: Mature BMP-4
     197 <300> PUBLICATION INFORMATION:
     198 <301> AUTHORs: WOZNEY, John M.
     199       ROSEN, Vicki
     200       CELESTE, Anthony J.
     201       MITSOCK, Lisa M.
     202       WHITTERS, Matthew J.
     203       KRIZ, Ronald W.
     204       HEWICK, Rodney M.
     205       WANG, Elizabeth A.
     206 <302> TITLE: Novel regulators of bone formation molecular clones
     207       and activities.
     208 <303> JOURNAL: Science
     209 <304> VOLUME: 242
     210 <305> ISSUE: 4885
     211 <306> PAGES: 1528-1534
     212 <307> DATE: 1988-12-16
     213 <308> DATABASE ACCESSION NO: Genbank/M22490
     214 <313> RELEVANT RESIDUES: 1 TO 116
     216 <300> PUBLICATION INFORMATION: 3
     217       Ser Pro Lys His His Ser Gln Arg Ala Arg Lys Lys Asn Lys Asn Cys
     218       1               5                   10                  15
     220       Arg Arg His Ser Leu Tyr Val Asp Phe Ser Asp Val Gly Trp Asn Asp
     221                       20                  25                  30
     223       Trp Ile Val Ala Pro Pro Gly Tyr Gln Ala Phe Tyr Cys His Gly Asp
E--> 224                       35                  40                  45
     239       WO 00/21998                                    PCT/IB99/01621
E--> 241                                        5
     244       Cys Pro Phe Pro Leu Ala Asp His Leu Asn Ser Thr Asn His Ala Ile
E--> 245           50                  55                  60
     247       Val Gln Thr Leu Val Asn Ser Val Asn Ser Ser Ile Pro Lys Ala Cys
E--> 248       65                  70                  75                  80
     250       Cys Val Pro Thr Glu Leu Ser Ala Ile Ser Met Leu Tyr Leu Asp Glu
     251                       85                  90                  95
     253       Tyr Asp Lys Val Val Leu Lys Asn Tyr Gln Glu Met Val Val Glu Gly
     254                   100                 105                 110
     256       Cys Gly Cys Arg
E--> 257       115
     259 <210> SEQ ID NO: 4
     261 <211> LENGTH: 139
     262 <212> TYPE: PRT
```

>(3097 ← This numeric identifier is mandatory whenever <308> has a response

delete misaligned number

RAW SEQUENCE LISTING   DATE: 05/14/2002
PATENT APPLICATION: US/09/806,368B   TIME: 16:26:47

Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

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263 <213> ORGANISM: Human
265 <220> FEATURE:
267 <221> NAME/KEY: CHAIN
268 <222> LOCATION: (1)..(139)
269 <223> OTHER INFORMATION: Mature BMP-7
271 <300> PUBLICATION INFORMATION:
273 <301> AUTHORs: OZKAYNAK, Engin
274       RUEGER, David C.
275       DRIER, Eric A.
276       CORBETT, Clare
277       RIDGE, Richard J.
278       SAMPATH, Kuber T.
279       OPPERMANN, Hermann
280 <302> TITLE: OP-1 cDNA encodes an osteogenic protein in the TGF-beta
281       family.
294       WO 00/21998 PCT/IB99/01621    delete
296       6
300 <303> JOURNAL: EMBO J.
301 <304> VOLUME: 9
302 <305> ISSUE: 7
303 <306> PAGES: 2085-2093
304 <307> DATE: 1990
305 <308> DATABASE ACCESSION NO: EMBL data library/X51801   ><309> mandatory
306 <313> RELEVANT RESIDUES: 1 TO 139                        numeric
308 <300> PUBLICATION INFORMATION: 4                         identifier
310     Ser Thr Gly Ser Lys Gln Arg Ser Gln Asn Arg Ser Lys Thr Pro Lys   and
311     1               5                   10                  15
313     Asn Gln Glu Ala Leu Arg Met Ala Asn Val Ala Glu Asn Ser Ser Ser   response
314                     20                  25                  30
316     Asp Gln Arg Gln Ala Cys Lys Lys His Glu Leu Tyr Val Ser Phe Arg
317                 35                  40                  45
319     Asp Leu Gly Trp Gln Asp Trp Ile Ile Ala Pro Glu Gly Tyr Ala Ala
320         50                  55                  60
322     Tyr Tyr Cys Glu Gly Glu Cys Ala Phe Pro Leu Asn Ser Tyr Met Asn
323     65          70                      75                  80  > misaligned
325     Ala Thr Asn His Ala Ile Val Gln Thr Leu Val His Phe Ile Asn Pro   number
326                     85                  90                  95
328     Glu Thr Val Pro Lys Pro Cys Cys Ala Pro Thr Gln Leu Asn Ala Ile
329                     100                 105                 110
331     Ser Val Leu Tyr Phe Asp Asp Ser Ser Asn Val Ile Leu Lys Lys Tyr
332                     115                 120                 125
334     Arg Asn Met Val Val Arg Ala Cys Gly Cys His
335                     130                 135
350     WO 00/21998                              PCT/IB99/01621
352                              7
355 <210> SEQ ID NO: 5                                        delete
357 <211> LENGTH: 119
358 <212> TYPE: PRT
359 <213> ORGANISM: Human
```

```
                RAW SEQUENCE LISTING              DATE: 05/14/2002
                PATENT APPLICATION:  US/09/806,368B     TIME: 16:26:47

                Input Set : A:\447.001.txt
                Output Set: N:\CRF3\05142002\I806368B.raw
```

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361 <220> FEATURE:
363 <221> NAME/KEY: CHAIN
364 <222> LOCATION: (1)..(119)
365 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th, 71st, 74th and
366       111th Met are modified to Met sulfoxide.
368 <400> SEQUENCE: 5
370     Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
371     1               5                   10                  15
373     Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
374                 20                  25                  30
376     Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
377                 35                  40                  45
379     Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
380             50                  55                  60
382     Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
383         65                  70                  75                  80
385     Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
386                 85                  90                  95
388     Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
389                 100                 105                 110
391     Val Glu Ser Cys Gly Cys Arg
392             115
407     WO 00/21998                                 PCT/IB99/01621
409                             8
411 <210> SEQ ID NO: 6
412 <211> LENGTH: 119
413 <212> TYPE: PRT
414 <213> ORGANISM: Human
416 <220> FEATURE:
417 <221> NAME/KEY: CHAIN
418 <222> LOCATION: (1)..(119)
419 <223> OTHER INFORMATION: Mature MP52 protein. Note : 30th and/or 71st
420       and/or 74th and/or 111th met are modified to
421       s-carboxymethyl Met.
423 <400> SEQUENCE: 6
425     Pro Leu Ala Thr Arg Gln Gly Lys Arg Pro Ser Lys Asn Leu Lys Ala
426     1               5                   10                  15
428     Arg Cys Ser Arg Lys Ala Leu His Val Asn Phe Lys Asp Met Gly Trp
429                 20                  25                  30
431     Asp Asp Trp Ile Ile Ala Pro Leu Glu Tyr Glu Ala Phe His Cys Glu
432                 35                  40                  45
434     Gly Leu Cys Glu Phe Pro Leu Arg Ser His Leu Glu Pro Thr Asn His
435             50                  55                  60
437     Ala Val Ile Gln Thr Leu Met Asn Ser Met Asp Pro Glu Ser Thr Pro
438         65                  70                  75                  80
440     Pro Thr Cys Cys Val Pro Thr Arg Leu Ser Pro Ile Ser Ile Leu Phe
441                 85                  90                  95
443     Ile Asp Ser Ala Asn Asn Val Val Tyr Lys Gln Tyr Glu Asp Met Val
444                 100                 105                 110
```

E--> 409 *(handwritten annotation: "delete" with line encircling lines 392–409)*

RAW SEQUENCE LISTING   DATE: 05/14/2002
PATENT APPLICATION: US/09/806,368B   TIME: 16:26:47
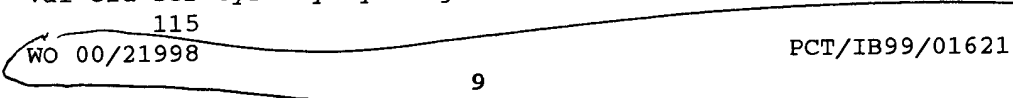
Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

        446   Val Glu Ser Cys Gly Cys Arg
        447   115
        464   WO 00/21998   PCT/IB99/01621
E--> 466   9

                    delete

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 05/14/2002
PATENT APPLICATION: US/09/806,368B   TIME: 16:26:48

Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

Invalid Line Length:
The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 162

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/806,368B

DATE: 05/14/2002
TIME: 16:26:48

Input Set : A:\447.001.txt
Output Set: N:\CRF3\05142002\I806368B.raw

```
L:6 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:8 M:259 W: Allowed number of lines exceeded, (1) GENERAL INFORMATION:
L:20 M:270 C: Current Application Number differs, Replaced Application Number
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:72 M:256 W: Invalid Numeric Header Field, Wrong PUBLICATION DATE:YYYY-MM-DD
L:78 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:1
L:123 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:125 M:259 W: Allowed number of lines exceeded, <213> ORGANISM:
L:154 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:2
M:332 Repeated in SeqNo=2
L:216 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:3
L:220 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3
M:332 Repeated in SeqNo=3
L:308 M:256 W: Invalid Numeric Header Field, Identifier <309> Expected, SEQ:4
L:323 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:4
M:332 Repeated in SeqNo=4
L:409 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:5
L:466 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:6
```